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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,886

DATE: 12/17/2001

TIME: 12:07:26

Input Set : N:\Crf3\RULE60\09825886.txt

Output Set: N:\CRF3\12172001\I825886.raw

3 <110> APPLICANT: Hovanessian, Ara
4 Callebaut, Christian
5 Krust, Bernard
6 Jacotot, Etienne
7 Muller, Sylviane
8 Briand, Jean-Paul
9 Guichard, Giles
11 <120> TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
12 THERAPEUTIC AND DIAGNOSTIC USES.
14 <130> FILE REFERENCE: 03495.0166-01000
16 <140> CURRENT APPLICATION NUMBER: 09/825,886
C--> 17 <141> CURRENT FILING DATE: 2001-07-26
19 <150> PRIOR APPLICATION NUMBER: 09/393,302
20 <151> PRIOR FILING DATE: 1999-09-10
22 <150> PRIOR APPLICATION NUMBER: PCT/EP98/01409
23 <151> PRIOR FILING DATE: 1998-03-12
25 <150> PRIOR APPLICATION NUMBER: 60/040,969
26 <151> PRIOR FILING DATE: 1997-03-12
28 <160> NUMBER OF SEQ ID NOS: 32
30 <170> SOFTWARE: PatentIn Ver. 2.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 30
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA
40 <400> SEQUENCE: 1
41 cgccgccatc atggtgaagc tcgcgaaggt 30
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 30
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA
51 <400> SEQUENCE: 2
52 gagagcgca gagatggaga tgggcagacg 30
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 30
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA
62 <400> SEQUENCE: 3
63 gcagcaccat gtcggcgccg gcggccaaag 30
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 22
67 <212> TYPE: DNA

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68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
73 <400> SEQUENCE: 4
74 cttcgggtgt acgtgctccg gg                                22
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 22
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
84 <400> SEQUENCE: 5
85 cctgagtgac tttgtaaggg ag                                22
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 21
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:
94     primer
96 <400> SEQUENCE: 6
97 ccgccggcgc gccagcctct g                                21
99 <210> SEQ ID NO: 7
100 <211> LENGTH: 21
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
107 <400> SEQUENCE: 7
108 gtcacatct tctccctcat c                                21
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 21
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
118 <400> SEQUENCE: 8
119 cgaccgcgga gcagcaccat g                                21
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 20
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
129 <400> SEQUENCE: 9
130 ggaaggttg aatccatcag                                20
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 40
134 <212> TYPE: PRT

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135 <213> ORGANISM: Human immunodeficiency virus
137 <400> SEQUENCE: 10
138 Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln
139 1 5 10 15
141 Arg Gly Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met
142 20 25 30
144 Arg Gln Ala His Cys Asn Ile Ser
145 35 40
147 <210> SEQ ID NO: 11
148 <211> LENGTH: 39
149 <212> TYPE: PRT
150 <213> ORGANISM: Human immunodeficiency virus
152 <400> SEQUENCE: 11
153 Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
154 1 5 10 15
156 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile Arg
157 20 25 30
159 Gln Ala His Cys Asn Leu Ser
160 35
162 <210> SEQ ID NO: 12
163 <211> LENGTH: 14
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 12
168 Lys Lys Leu Glu Leu Ser Glu Asn Arg Ile Phe Gly Gly Leu
169 1 5 10
171 <210> SEQ ID NO: 13
172 <211> LENGTH: 14
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 13
177 Lys Lys Leu Glu Leu Ser Asp Asn Arg Val Ser Gly Gly Leu
178 1 5 10
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 16
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 14
187 Lys Gln Gly Thr Glu Ile Asp Gly Arg Ser Ile Ser Leu Tyr Tyr Thr
188 1 5 10 15
191 <210> SEQ ID NO: 15
192 <211> LENGTH: 15
193 <212> TYPE: PRT
194 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 15
197 Lys Gly Tyr Ala Phe Ile Glu Phe Ala Ser Phe Glu Asp Ala Lys
198 1 5 10 15
201 <210> SEQ ID NO: 16
202 <211> LENGTH: 15

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```

203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 16
207 Lys Gly Tyr Ala Phe Ile Glu Phe Ala Ser Phe Glu Asp Ala Lys
208   1           5           10           15
211 <210> SEQ ID NO: 17
212 <211> LENGTH: 7
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <400> SEQUENCE: 17
217 Lys Ala Leu Glu Leu Thr Gly
218   1           5
221 <210> SEQ ID NO: 18
222 <211> LENGTH: 7
223 <212> TYPE: PRT
224 <213> ORGANISM: Homo sapiens
226 <400> SEQUENCE: 18
227 Lys Gln Gly Thr Glu Ile Asp
228   1           5
231 <210> SEQ ID NO: 19
232 <211> LENGTH: 10
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 19
237 Lys Val Thr Leu Asp Trp Ala Lys Pro Lys
238   1           5           10
241 <210> SEQ ID NO: 20
242 <211> LENGTH: 7
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 20
247 Lys Lys Leu Glu Leu Ser Glu
248   1           5
251 <210> SEQ ID NO: 21
252 <211> LENGTH: 16
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Xaa at position 8 is unknown
259 <400> SEQUENCE: 21
W--> 260 Lys Ser Leu Asp Leu Phe Asn Xaa Glu Val Thr Asn Leu Asn Asp Tyr
261   1           5           10           15
264 <210> SEQ ID NO: 22
265 <211> LENGTH: 707
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 22
270 Met Val Lys Leu Ala Lys Ala Gly Lys Asn Gln Gly Asp Pro Lys Lys
271   1           5           10           15

```

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```

273 Met Ala Pro Pro Pro Lys Glu Val Glu Glu Asp Ser Glu Asp Glu Glu
274                20                25                30
276 Met Ser Glu Asp Glu Glu Asp Asp Ser Ser Gly Glu Glu Val Val Ile
277                35                40                45
279 Pro Gln Lys Lys Gly Lys Lys Ala Ala Ala Thr Ser Ala Lys Lys Val
280                50                55                60
282 Val Val Ser Pro Thr Lys Lys Val Ala Val Ala Thr Pro Ala Lys Lys
283        65                70                75                80
285 Ala Ala Val Thr Pro Gly Lys Lys Ala Ala Ala Thr Pro Ala Lys Lys
286                85                90                95
288 Thr Val Thr Pro Ala Lys Ala Val Thr Thr Pro Gly Lys Lys Gly Ala
289                100               105               110
291 Thr Pro Gly Lys Ala Leu Val Ala Thr Pro Gly Lys Lys Gly Ala Ala
292                115               120               125
294 Ile Pro Ala Lys Gly Ala Lys Asn Gly Lys Asn Ala Lys Lys Glu Asp
295        130               135               140
297 Ser Asp Glu Glu Glu Asp Asp Asp Ser Glu Glu Asp Glu Glu Asp Asp
298 145                150                155                160
300 Glu Asp Glu Asp Glu Asp Glu Asp Glu Ile Glu Pro Ala Ala Met Lys
301                165                170                175
303 Ala Ala Ala Ala Ala Pro Ala Ser Glu Asp Glu Asp Asp Glu Asp Asp
304                180                185                190
306 Glu Asp Asp Glu Asp Asp Asp Asp Asp Glu Glu Asp Asp Ser Glu Glu
307                195                200                205
309 Glu Ala Met Glu Thr Thr Pro Ala Lys Gly Lys Lys Ala Ala Lys Val
310        210                215                220
312 Val Pro Val Lys Ala Lys Asn Val Ala Glu Asp Glu Asp Glu Glu Glu
313 225                230                235                240
315 Asp Asp Glu Asp Glu Asp Asp Asp Asp Asp Glu Asp Asp Glu Asp Asp
316                245                250                255
318 Asp Asp Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Pro
319                260                265                270
321 Val Lys Glu Ala Pro Gly Lys Arg Lys Lys Glu Met Ala Lys Gln Lys
322        275                280                285
324 Ala Ala Pro Glu Ala Lys Lys Gln Lys Val Glu Gly Thr Glu Pro Thr
325        290                295                300
327 Thr Ala Phe Asn Leu Phe Val Gly Asn Leu Asn Phe Asn Lys Ser Ala
328 305                310                315                320
330 Pro Glu Leu Lys Thr Gly Ile Ser Asp Val Phe Ala Lys Asn Asp Leu
331                325                330                335
333 Ala Val Val Asp Val Arg Ile Gly Met Thr Arg Lys Phe Gly Tyr Val
334                340                345                350
336 Asp Phe Glu Ser Ala Glu Asp Leu Glu Lys Ala Leu Glu Leu Thr Gly
337        355                360                365
339 Leu Lys Val Phe Gly Asn Glu Ile Lys Leu Glu Lys Pro Lys Gly Lys
340        370                375                380
342 Asp Ser Lys Lys Glu Arg Asp Ala Arg Thr Leu Leu Ala Lys Asn Leu
343 385                390                395                400
345 Pro Tyr Lys Val Thr Gln Asp Glu Leu Lys Glu Val Phe Glu Asp Ala

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VERIFICATION SUMMARY

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:260 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:260 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21